Amendments to the Specification:

Please replace the paragraph on page 1, immediately following the Title Header, with the following amended paragraph

--This application is a continuation-in-part of <u>U.S.</u> Application No. 09/645,593 filed August 25, 2000 (now U.S. Patent No. 6,777,591), ~~now allowed,~~ and ~~based on~~ claims benefit from U.S. Provisional Application Nos. 60/151,044, filed August 27, 1999 and 60/161,722, filed October 27, 1999.--

Please replace the paragraph beginning on page 11, line 12 to page 12, line 7, with the following amended paragraph:

--The term "sequence that has substantial sequence homology" means those nucleic acid sequences which have slight or inconsequential sequence variations from the sequences in (a) or (b), i.e., the sequences function in substantially the same manner and are capable of driving seed specific expression of non-native nucleic acid sequences. The variations may be attributable to local mutations or structural modifications. Nucleic acid sequences having substantial homology include nucleic acid sequences having at least 65%, more preferably at least 85%, and most preferably 90-95% identity with the nucleic acid sequences as shown in Figure 1 (SEQ.ID.NO.:1), Figure 2 (SEQ.ID.NO.:4), Figure 3 (SEQ.ID.NO.:6) or Figure 4 (SEQ.ID.NO.:8). Sequence identity can be calculated according to methods known in the art. Sequence identity is most preferably assessed by the algorithm of BLAST version 2.1 advanced search. BLAST is a series of programs that are available online ~~at~~ ~~http://~~www.ncbi.nlm.nih.gov/BLAST. The advanced blast search (~~http://~~www.ncbi.nlm.nih.gov/blast/blast.cgi?Jform=1) is set to default parameters. (~~ie~~ i.e., Matrix BLOSUM62; Gap existence cost 11; Per residue gap cost 1; Lambda ratio 0.85 default). References to BLAST searches are: Altschul, S.F., Gish, W., Miller, W., Myers, E.W. & Lipman, D.J. (1990) "Basic local alignment search tool." J. Mol. Biol. 215:403410; Gish, W. & States, D.J. (1993) "Identification of protein coding regions by database similarity

search." Nature Genet. 3:266272; Madden, T.L., Tatusov, R.L. & Zhang, J. (1996) "Applications of network BLAST server" Meth. Enzymol. 266:131_141; Altschul, S.F., Madden, T.L., Schäffer, A.A., Zhang, J., Zhang, Z., Miller, W. & Lipman, D.J. (1997) "Gapped BLAST and PSI_BLAST: a new generation of protein database search programs." Nucleic Acids Res. 25:33893402; Zhang, J. & Madden, T.L. (1997) "PowerBLAST: A new network BLAST application for interactive or automated sequence analysis and annotation." Genome Res. 7:649656.--